



1

SEQUENCE LISTING

RECEIVED

MAY 10 2002

TECH CENTER 1600/2900

<110> Dahlqvist, Andres
Stahl, Ulf
Lenman, Marit
Banas, Antoni
Ronne, Hans

<120> A new class of enzymes in the biosynthetic pathway for the production of triacylglycerol and recombinant DNA molecules encoding these enzymes

<130> BASFnae337799PCT1-15

<140> US 09/537,710

<141> 2000-03-30

<150> EP 99106656.4

<151> 1999-04-01

<160> 31

<170> WordPerfect version 6.1

<210> 1

<211> 1986

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> (1)..(1983)

<400> 1

atg ggc aca ctg ttt cga aga aat gtc cag aac caa aag agt gat tct 48
Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
1 5 10 15

gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga 96
Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
20 25 30

aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt 144
Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
35 40 45

att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg 192
Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
50 55 60

aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg 240
Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
65 70 75 80

att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt 288
Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
85 90 95

ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt	336
Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe	
100 105 110	
gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt	384
Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val	
115 120 125	
ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac	432
Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn	
130 135 140	
tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt	480
Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly	
145 150 155 160	
aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta	528
Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val	
165 170 175	
atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att	576
Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile	
180 185 190	
gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg	624
Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp	
195 200 205	
gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg	672
Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp	
210 215 220	
ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac	720
Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn	
225 230 235 240	
ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc	768
Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile	
245 250 255	
gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att	816
Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile	
260 265 270	
ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt	864
Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu	
275 280 285	
gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag	912
Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys	
290 295 300	
gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta	960
Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu	
305 310 315 320	
att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg	1008
Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp	
325 330 335	

Cl
Cont

gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt 1056
 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
 340 345 350

aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc 1104
 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
 355 360 365

gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc 1152
 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
 370 375 380

att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca 1200
 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
 385 390 395 400

aga att gag aga gta aaa atg tta caa acg tgg ggt ggt ata cca tca 1248
 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
 405 410 415

atg cta cca aag gga gaa gag gtc att tgg ggg gat atg aag tca tct 1296
 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
 420 425 430

tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att 1344
 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
 435 440 445

cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg 1392
 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
 450 455 460

aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa 1440
 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
 465 470 475 480

aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa 1488
 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
 485 490 495

gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg 1536
 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
 500 505 510

gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac 1584
 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
 515 520 525

ggg gtg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat 1632
 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
 530 535 540

gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag caa cct 1680
 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
 545 550 555 560

gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca 1728
 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575

Sub D

C1 Cont

atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga 1776
Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
580 585 590

att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat 1824
Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
595 600 605

ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc 1872
Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
610 615 620

gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat 1920
Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
625 630 635 640

ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag 1968
Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
645 650 655

atg ccc ttc cca atg taa 1986
Met Pro Phe Pro Met
660

<210> 2
<211> 661
<212> PRT
<213> Saccharomyces cerevisiae

<400> 2

Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
1 5 10 15

Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
20 25 30

Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
35 40 45

Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
50 55 60

Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
65 70 75 80

Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
85 90 95

Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
100 105 110

Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
115 120 125

Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
130 135 140

Sub D1

C1
Cont

Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
 145 150 155 160
 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
 165 170 175
 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
 180 185 190
 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
 195 200 205
 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
 210 215 220
 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
 225 230 235 240
 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
 245 250 255
 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
 260 265 270
 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
 275 280 285
 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
 290 295 300
 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
 305 310 315 320
 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
 325 330 335
 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
 340 345 350
 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
 355 360 365
 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
 370 375 380
 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
 385 390 395 400
 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
 405 410 415
 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
 420 425 430
 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
 435 440 445
 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
 450 455 460

But DI

C1
Cont

Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
465 470 475 480

Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
485 490 495

Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
500 505 510

Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
515 520 525

Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
530 535 540

Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
545 550 555 560

Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
565 570 575

Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
580 585 590

Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
595 600 605

Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
610 615 620

Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
625 630 635 640

Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
645 650 655

Met Pro Phe Pro Met
660

<210> 3
<211> 2312
<212> DNA
<213> Schizosaccharomyces pombe

<400> 3

atggcgctctt ccaagaagag caaaactcat aagaaaaaga aagaagtcaa atctcctatc 60
gacttaccaa attcaaagaa accaactcgc gctttgagtg agcaaccttc agcgtccgaa 120
acacaatctg tttcaaataa atcaagaaaa tctaaatttg gaaaaagatt gaattttata 180
ttgggcgcta ttttggaat atgcggtgct ttttttttcg ctgttgagaga cgacaatgct 240
gttttcgacc ctgctacgtt agataaattt gggaatatgc taggctcttc agacttggtt 300
gatgacatta aaggatattt atcttataat gtgtttaagg atgcaccttt tactacggac 360
aagccttcgc agtctcctag cggaaatgaa gttcaagttg gtcttgatat gtacaatgag 420
ggatatcgaa gtgaccatcc tgttattatg gttccttggtg ttatcagctc aggattagaa 480
agttggtcgt ttaataattg ctcgattcct tacttttagga aacgtctttg gggtagctgg 540
tctatgctga aggcaatgtt ccttgacaag caatgctggc ttgaacattt aatgcttgat 600
aaaaaaaccg gcttgatcc gaagggaatt aagctgcgag cagctcaggg gtttgaagca 660

gctgattttt	ttatcacggg	ctattggatt	tggagtaaag	taattgaaaa	ccttgctgca	720
attgggttatg	agcctaataa	catgttaagt	gcttcttacg	attggcggtt	atcatatgca	780
aatttagagg	aacgtgataa	atatttttca	aagttaaaaa	tgttcattga	gtacagcaac	840
attgtacata	agaaaaaggt	agtgttgatt	tctcactcca	tgggttcaca	ggttacgtac	900
tattttttta	agtgggttga	agctgagggc	tacggaaatg	gtggaccgac	ttgggttaat	960
gatcatattg	aagcatttat	aatgttgagt	ctcgatgggt	gtttgactac	gtttctaact	1020
tttgaataga	tatcgggatc	tttgattgga	gcacccaaaa	cagtggcagc	gcttttatcg	1080
gggtgaaatga	aagatacagg	tattgtaatt	acattaaaca	tgtaaatatt	taatttttgc	1140
taaccgtttt	aagctcaatt	gaatcagttt	tcgggtctatg	ggtaagcaat	aaattgttga	1200
gatttggttac	taattttactg	tttagtttgg	aaaaattttt	ttcccgttct	gaggtatatt	1260
caaaaataca	aatgtgctct	actttttcta	acttttaata	gagagccatg	atggttcgca	1320
ctatgggagg	agttagtctt	atgcttcccta	aaggaggcga	tggtgtatgg	ggaaatgccca	1380
gttgggtaag	aaatatgtgc	tgtaaatttt	ttattaatat	ttaggctcca	gatgatctta	1440
atcaaacaaa	tttttccaat	ggtgcaatta	ttcgatatag	agaagacatt	gataaggacc	1500
acgatgaatt	tgacatagat	gatgcattac	aattttttaa	aaatgttaca	gatgacgatt	1560
ttaaagtcac	gctagcgaaa	aattattccc	acggctcttgc	ttggactgaa	aaagaagtgt	1620
taaaaaataa	cgaaatgccg	tctaaatgga	taaatccgct	agaagtaaga	acattaaagt	1680
tactaaatta	tactaaccga	aatagactag	tcttccttat	gctcctgata	tgaaaattta	1740
ttgcgttcac	ggggtcggaa	aaccaactga	gagaggttat	tattatacta	ataatcctga	1800
ggggcaacct	gtcattgatt	cctcgggtta	tgatggaaca	aaagttgaaa	atgtgagaga	1860
atztatgttt	caaacattct	attaactgtt	ttattagggt	attgttatgg	atgatgggtga	1920
tggaacttta	ccaatattag	cccttggttt	ggtgtgcaat	aaagtttggc	aaacaaaaag	1980
gtttaatcct	gctaatacaa	gtatcacaaa	ttatgaaatc	aagcatgaac	ctgctgcggt	2040
tgatctgaga	ggaggacctc	gctcggcaga	acacgtcgat	atacttggac	attcagagct	2100
aaatgtatgt	tcattttacc	ttacaaattt	ctattactaa	ctcttgaaat	aaggaaatta	2160
ttttaaaagt	ttcatcaggc	catgggtgact	cggtaacaaa	ccgttatata	tcagatatcc	2220
agtacggaca	taagttttgt	agattgcaat	taactaacta	accgaacagg	gaaataataa	2280
atgagataaa	tctcgataaa	cctagaat	aa			2312

<210> 4

<211> 3685

<212> DNA

<213> Arabidopsis thaliana

<400> 4

atgccccctta	ttcatcggaa	aaagccgacg	gagaaacat	cgacgccgcc	atctgaagag	60
gtgggtgcacg	atgaggattc	gcaaaagaaa	ccacacgaat	cttccaaatc	ccaccataag	120
aaatcgaagc	gaggagggaa	gtggctcgtc	atcgattctt	gttgttgggt	cattgggtgt	180
gtgtgtgtaa	cctggtgggt	tcttctcttc	ctttacaacg	caatgcctgc	gagcttccct	240
cagtagttaa	cggagggaat	cacgggtcct	ttgcctgacc	cgcccggtgt	taagctcaaa	300
aaagaaggtc	ttaaggcgaa	acatcctgtt	gtcttcattc	ctgggattgt	caccgggtggg	360
ctcgagcttt	gggaaggcaa	acaatgcgct	gatggtttat	ttagaataacg	tttgtggggt	420
ggaacttttg	gtgaagtcta	caaaagggtga	gctcaacaat	tctcaetctt	cctttatatt	480
gggattttgga	ttggatctga	tgagatcacg	cacttggtgc	ttcttcaaca	tactcaaac	540
tttaattcca	tgtttgtctg	tcttactctt	tacttttttt	tttttttgat	gtgaaacgct	600
attttcttaa	gagactattt	ctgtatgtgt	aaggtaagcg	ttccaaggac	gtaattggct	660
tggactattt	ctgtttgatt	gttaacttta	ggatataaaa	tagctgcctt	ggaatttcaa	720
gtcatcttat	tgccaaatct	gttgctagac	atgccctaga	gtccgttcat	aacaagttac	780
ttcctttact	gtcgttgctg	gtagatttag	ctttgtgtag	cgtataatga	agtagtggtt	840
tatgttttgt	tggaataga	gaagttctaa	ctacatctgt	ggaaagtgtg	ttcaggctgt	900
gatagaggac	tgttgcttta	ttattcaact	atgtatatgt	gtaattaaag	ctagttcctt	960
tttgatcttt	cagctcaatg	tgcttttctc	aatttttttc	tcaatttcaa	agtttcacat	1020
cgagtttatt	cacatgtctt	gaatttcgtc	catcctcggt	ctgttatcca	gctttgaact	1080
cctcccgacc	ctgctatgga	tatatataaa	aaaaagtgtt	ttgtgggttg	catctttgtt	1140
acgatctgca	tcttctcttc	tcggctcagt	gttcgatgtt	ttgctatggt	agagatgggc	1200
aatgtttatt	ttgatggtaa	caggtgtata	gttgatagta	tcttaactaa	tcaattatct	1260
ctttgattca	ggcctctatg	ttgggtggaa	cacatgtcac	ttgacaatga	aactgggttg	1320

C1
Cm

gatccagctg gtattagagt tgcagctgta tcaggactcg tggctgctga ctactttgct 1380
cctggctact ttgtctgggc agtgctgatt gctaaccttg cacatattgg atatgaagag 1440
aaaaatatgt acatggctgc atatgactgg cggctttcgt ttcagaacac agagggtcctt 1500
ttctcatcgt tctttctatt attctgttcc atgttacgtt tctttcttca ttacttaagg 1560
cttaaatatg tttcatgttg aattaatagg tacgtgatca gactcttagc cgtatgaaaa 1620
gtaatataga gttgatgggt tctaccaacg gtggaaaaaa agcagttata gttccgcatt 1680
ccatgggggt cttgtatttt ctacatttta tgaagtggtg tgaggcacca gctcctctgg 1740
gtggcggggg tgggccagat tgggtgtgcaa agtatattaa ggcgggtgatg aacattgggtg 1800
gaccatttct tgggtgttcca aaagctgttg cagggtcttt ctctgctgaa gcaaaggatg 1860
ttgcagttgc cagggtattga atatctgctt atacttttga tgatcagaac cttggctctg 1920
gaactcaaag ttattctact aaatatcaat tctaataaca ttgctatatt atcgctgcaa 1980
ctgacattgg ttgattattt ttgctgctta tgtaactgaa actctcttga gattagacaa 2040
atgatgaatt gataattcct acgcatttgc ctgtgatgac cagtttctta gcttcgacga 2100
taacatttgt catactgtct tttggagggc attgaatttt gctatggaaa gcgctggagc 2160
ttccatgctt gcattcttta ccaatttagc ttattctgct tctttcaatt ttcttgata 2220
tgcactcatg gtcttttatt tcttcttaat taaagactcg ttggattagt tgctctatta 2280
gtcacttggg tccttaatat agaactttac tttcttcgaa aattgcagag cgattgcccc 2340
aggattctta gacaccgata tatttagact tcagaccttg cagcatgtaa tgagaatgac 2400
acgcacatgg gactcaacaa tgtctatgtt accgaaggga ggtgacacga tatggggcgg 2460
gcttgattgg tcaccggaga aaggccacac ctgttggtggg aaaaagcaaa agaacaacga 2520
aacttggtgg gaagcagggtg aaaacggagt ttccaagaaa agtcctgtta actatggaag 2580
gatgatatct tttgggaaag aagtagcaga ggctgcgcca tctgagatta ataatttga 2640
ttttcgagta aggacatata aatcataata aaccttgtag attttgtgat tgtatgatga 2700
atatctgtac attttatctg gtgaagggtg gtgtcaaagg tcagagtatc ccaaatcaca 2760
cctgtcgtga cgtgtggaca gagtaccatg acatgggaat tgctgggatc aaagctatcg 2820
ctgagtataa ggtctacact gctgggtgaag ctatagatct actacattat gttgctccta 2880
agatgatggc gcgtgggtgcc gctcatttct ctatgggaat tgctgatgat ttggatgaca 2940
ccaagtatca agatcccaaa tactgggtcaa atccgttaga gacaaagtaa gtgatttctt 3000
gattccaact gtatccttcg tctgatgca ttatcagtct ttttgttttc ggtcttgttg 3060
gatatggttt tcagctcaaa gcttacaaaag ctgtttctga gcctttctca aaaaggcttg 3120
ctcagtaata ttgaggtgct aaagttagata catgtgactc ttgcttataa atcctccgtt 3180
tgggttggte tgctttttca gattaccgaa tgctcctgag atggaaatct actcattata 3240
cggagtgggg ataccaacgg aacgagcata cgtatacaag cttaaccagt ctcccgacag 3300
ttgcatcccc tttcagatat tcacttctgc tcacgaggag gacgaagata gctgtctgaa 3360
agcaggagtt tacaatgtgg atggggatga aacagtaccg gtcctaagtg ccgggtacat 3420
gtgtgcaaaa gcgtggcgtg gcaagacaag attcaacctt tccggaatca agacttatat 3480
aagagaatac aatcactctc cgccggctaa cctgttgga gggcgcgagg cgagagtggt 3540
tgcccatgtt gatatcatgg gaaactttgc tttgatcgaa gatatcatga ggggtgccc 3600
cggaggtaac ggggtctgata taggacatga ccagggtccac tctggcatat ttgaatgggtc 3660
ggagcgtatt gacctgaagc tgtga 3685

<210> 5

<211> 2427

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> Unsure

<222> 1..2427

<223> n is g, c, a, t, or u.

<400> 5

agaaacagct ctttgtctct ctgcactgat ctaacaatcc ctaatctgtg ttctaaattc 60
ctggacgaga tttgacaaag tccgtatagc ttaacctggt ttaatttcaa gtgacagata 120
tgcccttat tcatcggaag aagccgacgg agaaaccatc gacgcgcgca tctgaagagg 180
tgggtgcacga tgaggattcg caaaagaaac cacacgaatc ttccaaatcc caecataaga 240
aatcgaacgg aggagggaa ggtcgtgca tcgattcttg ttgttgggtc attgggtgtg 300

tgtgtgtaac ctggtggttt ctctcttcc ttacaaacgc aatgcctgcg agcttcctc 360
 agtatgtaac ggagcgaatc acgggtcctt tgcctgaccc gcccggtgtt aagctcaaaa 420
 aaagaaggtc ttaaggcgaa acatcctgtt gtcttcattc ctgggattgt caccggtggg 480
 ctcgagcttt gggaaggcaa acaatgcgct gatggtttat ttagaaaacg tttgtgggg 540
 ggaacttttg gtgaagtcta caaaagcct ctatgttggg tggaaacacat gtcacttgac 600
 aatgaaactg ggttggatcc agctgttatt agagttcgag ctgtatcagg actcgtggct 660
 gctgactact ttgtccttgg ctactttgtc tgggcagtgc tgattgctaa ccttgacacat 720
 attggatatg aagagaaaaa tatgtacatg gctgcatatg actggcggct ttcgtttcag 780
 aacacagagg tactgtatca gactcttagc cgtatgaaaa gtaatataga gttgatgggt 840
 tctaccaacg gtggaaaaaa agcagttata gttccgcatt ccatgggggt cttgtatttt 900
 ctacatttta tgaagtgggt tgaggcacca gctcctctgg gtggcggggg tgggccagat 960
 tgggtgtgcaa agtatattaa ggcggtgatg aacattgggtg gaccatttct tgggtgtcca 1020
 aaagctgttg cagggccttt ctctgctgaa gcaaaggatg ttgcagttgc cagagcgatt 1080
 gccccaggat tcttagacac cgatatattt agacttcaga ccttgacaga tgtaatgaga 1140
 atgacacgca catgggactc aacaatgtct atgttaccga agggaggtga cacgatattg 1200
 ggccgggttg attggtcacc ggagaaaaggc cacacctgtt gtgggaaaaa gcaaaagaac 1260
 aacgaaactt gtggtgaagc aggtgaaaac gtagtttcca agaaaagtcc tgttaactat 1320
 ggaaggatga tatcttttgg gaaagaagta gcagaggctg cgccatctga gattaataat 1380
 attgattttc gaggtgctgt caaaggctcag agtatcccaa atcacacctg tcgtgacgtg 1440
 tggacagagt accatgacat gggaattgct gggatcaaag ctatcgctga gtataaggct 1500
 tacactgctg gtgaagctat agatctacta cattatgttg ctctaagat gatggcgcgt 1560
 ggtgccgctc atttctctta tgggaattgct gatgatttgg atgacaccaa gtatcaagat 1620
 cccaaatact ggtcaaatcc gttagagaca aaattaccga atgctcctga gatggaaatc 1680
 tactcattat acggagtggg gataccaacg gaacgagcat acgtatacaa gcttaaccag 1740
 tctcccgaca gttgcatccc ttttcagata ttcacttctg ctcacgagga ggacgaagat 1800
 agctgtctga aagcaggagt ttacaatgtg gatgggatg aaacagtacc cgtcctaagt 1860
 gccgggtaca tgtgtgcaaa agcgtggcgt ggcaagacaa gattcaacc ttcgggaatc 1920
 aagacttata taagagaata caatcactct ccgccggeta acctgttggg agggcgcggg 1980
 acgcagagtg gtgcccattg tgatatcatg ggaaactttg ctttgatcga agatatcatg 2040
 agggttgccg ccggaggtaa cgggtctgat ataggacatg accagggtcca ctctggcata 2100
 tttgaatggt cggagcgtat tgacctgaag ctgtgaatat catgatctct ttaagctgtc 2160
 ctgtcagctt atgtgaatcc aatactttga aagagagatc atcatcaatt catcatcatc 2220
 gtcacatca tgatgctcaa ctcacaaaga agcctgagaa tgatactttg gtgcgaaatt 2280
 ctcaatacct ctttaatat cttattgaat gtaaattata caatcctatc taatgtttga 2340
 acgataacac aaaacttgct gcngccatgt ttgtttgtct tgtcaaaagc atcaatttgt 2400
 gggttaaaaa aaaaaaaaaa aaaaaaa 2427

<210> 6

<211> 671

<212> PRT

<213> Arabidopsis thaliana

<400> 6

Met Pro Leu Ile His Arg Lys Lys Pro Thr Glu Lys Pro Ser Thr Pro
 1 5 10 15
 Pro Ser Glu Glu Val Val His Asp Glu Asp Ser Gln Lys Lys Pro His
 20 25 30
 Glu Ser Ser Lys Ser His His Lys Lys Ser Asn Gly Gly Gly Lys Trp
 35 40 45
 Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr
 50 55 60
 Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro
 65 70 75 80

Gln Tyr Val Thr Glu Arg Ile Thr Gly Pro Leu Pro Asp Pro Pro Gly
 85 90 95
 Val Lys Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe
 100 105 110
 Ile Pro Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln
 115 120 125
 Cys Ala Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Gly
 130 135 140
 Glu Val Tyr Lys Arg Pro Leu Cys Trp Val Glu His Met Ser Leu Asp
 145 150 155 160
 Asn Glu Thr Gly Leu Asp Pro Ala Gly Ile Arg Val Arg Ala Val Ser
 165 170 175
 Gly Leu Val Ala Ala Asp Tyr Phe Ala Pro Gly Tyr Phe Val Trp Ala
 180 185 190
 Val Leu Ile Ala Asn Leu Ala His Ile Gly Tyr Glu Glu Lys Asn Met
 195 200 205
 Tyr Met Ala Ala Tyr Asp Trp Arg Leu Ser Phe Gln Asn Thr Glu Val
 210 215 220
 Arg Asp Gln Thr Leu Ser Arg Met Lys Ser Asn Ile Glu Leu Met Val
 225 230 235 240
 Ser Thr Asn Gly Gly Lys Lys Ala Val Ile Val Pro His Ser Met Gly
 245 250 255
 Val Leu Tyr Phe Leu His Phe Met Lys Trp Val Glu Ala Pro Ala Pro
 260 265 270
 Leu Gly Gly Gly Gly Gly Pro Asp Trp Cys Ala Lys Tyr Ile Lys Ala
 275 280 285
 Val Met Asn Ile Gly Gly Pro Phe Leu Gly Val Pro Lys Ala Val Ala
 290 295 300
 Gly Leu Phe Ser Ala Glu Ala Lys Asp Val Ala Val Ala Arg Ala Ile
 305 310 315 320
 Ala Pro Gly Phe Leu Asp Thr Asp Ile Phe Arg Leu Gln Thr Leu Gln
 325 330 335
 His Val Met Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu
 340 345 350
 Pro Lys Gly Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu
 355 360 365
 Lys Gly His Thr Cys Cys Gly Lys Lys Gln Lys Asn Asn Glu Thr Cys
 370 375 380
 Gly Glu Ala Gly Glu Asn Gly Val Ser Lys Lys Ser Pro Val Asn Tyr
 385 390 395 400

C1
 Cont

Gly Arg Met Ile Ser Phe Gly Lys Glu Val Ala Glu Ala Ala Pro Ser
 405 410 415
 Glu Ile Asn Asn Ile Asp Phe Arg Gly Ala Val Lys Gly Gln Ser Ile
 420 425 430
 Pro Asn His Thr Cys Arg Asp Val Trp Thr Glu Tyr His Asp Met Gly
 435 440 445
 Ile Ala Gly Ile Lys Ala Ile Ala Glu Tyr Lys Val Tyr Thr Ala Gly
 450 455 460
 Glu Ala Ile Asp Leu Leu His Tyr Val Ala Pro Lys Met Met Ala Arg
 465 470 475 480
 Gly Ala Ala His Phe Ser Tyr Gly Ile Ala Asp Asp Leu Asp Asp Thr
 485 490 495
 Lys Tyr Gln Asp Pro Lys Tyr Trp Ser Asn Pro Leu Glu Thr Lys Leu
 500 505 510
 Pro Asn Ala Pro Glu Met Glu Ile Tyr Ser Leu Tyr Gly Val Gly Ile
 515 520 525
 Pro Thr Glu Arg Ala Tyr Val Tyr Lys Leu Asn Gln Ser Pro Asp Ser
 530 535 540
 Cys Ile Pro Phe Gln Ile Phe Thr Ser Ala His Glu Glu Asp Glu Asp
 545 550 555 560
 Ser Cys Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val
 565 570 575
 Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys
 580 585 590
 Thr Arg Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn
 595 600 605
 His Ser Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly
 610 615 620
 Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met
 625 630 635 640
 Arg Val Ala Ala Gly Gly Asn Gly Ser Asp Ile Gly His Asp Gln Val
 645 650 655
 His Ser Gly Ile Phe Glu Trp Ser Glu Arg Ile Asp Leu Lys Leu
 660 665 670

<210> 7
 <211> 643
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS

C1
Cont

<222> (1)..(402)

<221> Unsure

<222> 1.. 643

<223> n is g, a, c, t or u.

<400> 7

cgg gag aaa ata gct gct ttg aag ggg ggt gtt tac tta gcc gat ggt 48
 Arg Glu Lys Ile Ala Ala Leu Lys Gly Gly Val Tyr Leu Ala Asp Gly
 1 5 10 15

gat gaa act gtt cca gtt ctt agt gcg ggc tac atg tgt gcg aaa gga 96
 Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly
 20 25 30

tgg cgt ggc aaa act cgt ttc agc cct gcc ggc agc aag act tac gtg 144
 Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
 35 40 45

aga gaa tac agc cat tcg cca ccc tct act ctc ctg gaa ggc agg ggc 192
 Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
 50 55 60

acc cag agc ggt gca cat gtt gat ata atg ggg aac ttt gct cta att 240
 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
 65 70 75 80

gag gac gtc atc aga ata gct gct ggg gca acc ggt gag gaa att ggt 288
 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
 85 90 95

ggc gat cag gtt tat tca gat ata ttc aag tgg tca gag aaa atc aaa 336
 Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys
 100 105 110

ttg aaa ttg taa cct atg gga agt taa aga agt gcc gac ccg ttt att 384
 Leu Lys Leu Pro Met Gly Ser Arg Ser Ala Asp Pro Phe Ile
 115 120 125

gcg ttc caa agt gtc ctg cctgagtgca actctggatt ttgcttaaat 432
 Ala Phe Gln Ser Val Leu
 130 134

attgtaattt ttcacgcttc attcgtccct ttgtcaaatt tacatttgac aggacgccaa 492

tgcgatacga tggtgtaccg ctattttcag cattgtatat taaactgtac aggtgtaagt 552

tgcatttgcc agctgaaatt gtgtagtcgt tttctttacg atttaatanc aagtggcgga 612

gcagtgcccc aagcnaaaaa aaaaaaaaaa a 643

<210> 8

<211> 115

<212> PRT

<213> Zea mays

<400> 8

Arg Glu Lys Ile Ala Ala Leu Lys Gly Gly Val Tyr Leu Ala Asp Gly
 1 5 10 15
 Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly
 20 25 30
 Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
 35 40 45
 Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
 50 55 60
 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
 65 70 75 80
 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
 85 90 95
 Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys
 100 105 110
 Leu Lys Leu
 115

<210> 9
 <211> 616
 <212> DNA
 <213> Neurospora crassa

 <220>
 <221> Unsure
 <222> 1..616
 <223> n is g, c, a, t, or u.

 <400> 9

ggtggcgaag acganggcgg aagttggagg ctaacgagaa tgacnctcgg agatggatct 60
 accctctaga gacacgacta ccnttgcacc cagcctcaag gtntacngtt tntatgggta 120
 ggaagccgac ggagcgagcc tacatctatc tggcgcccga tcccgggacg acaacgcatac 180
 tttagatgac gatcgatacg actttgactn aggggcacat tgaccacggg gtgattttgg 240
 gcgaaggcga tggcacagtg aaccttatga gtttggggta cctgtgcaat aaggggtgga 300
 aaatgaagag atacaatcct gcgggctcaa aaataaccgt ggtcgagatg ccgcatgaac 360
 cagaacgggt caatccgaga ggagggccga atacggcgga tcacgtggat attctaggaa 420
 ggcagaatct aaacgagtac attcttaaag tggcggcagg tcgaggcgat acaattgagg 480
 attttattac tagtaatatt cttaaataatg tagaaaaggt tgaaatttat gaagagtaat 540
 taaatacggc acatagggtta ctcaatagta tgactaatta aaaaaaaatt ttttttctaa 600
 aaaaaaaaaa aaaaaa 616

<210> 10
 <211> 1562
 <212> DNA
 <213> Arabidopsis thaliana

<400> 10

atgaaaaaaaa tatcttcaca ttattcggta gtcatagcga tactcgttgt ggtgacgatg 60

acctcgatgt	gtcaagctgt	gggtagcaac	gtgtaccctt	tgattctggt	tccaggaaac	120
ggaggttaacc	agctagaggt	acggctggac	agagaataca	agccaagtag	tgtctggtgt	180
agcagctggt	tatatccgat	tcataagaag	agtgggtggt	ggtttaggct	atggttcgat	240
gcagcagtggt	tattgtctcc	cttcaccagg	tgcttcagcg	atcgaatgat	gttgtactat	300
gaccctgatt	tggatgatta	ccaaaatgct	cctgggtgtcc	aaaccgggt	tcctcatttc	360
gggtcgacca	aatcacttct	atacctcgac	cctcgctccc	ggttagtact	ttccaagata	420
tatcattttg	ggacatttgc	ataatgaaca	aaatagacat	aaatttgggg	gattattggt	480
atatcaatat	ccattttatat	gctagtcggt	aatgtgagt	ttatgttagt	atagttaatg	540
tgagtgttat	gtgattttcc	attttaaatg	aagctagaaa	gttgtcgttt	aataatgttg	600
ctatgtcatg	agaattataa	ggacactatg	taaatgtagc	ttaataataa	ggtttgattt	660
gcagagatgc	cacatcttac	atggaacatt	tggtgaaagc	tctagagaaa	aaatgcgggt	720
atgttaacga	ccaaaccatc	ctaggagctc	catatgattt	caggtagcgc	ctggctgctt	780
cgggccaccc	gtcccgtgta	gcctcacagt	tcctacaaga	cctcaaacia	ttggtggaaa	840
aaactagcag	cgagaacgaa	ggaaagccag	tgatactcct	ctcccatagc	ctaggaggac	900
ttttcgtcct	ccatttcctc	aaccgtacca	ccccttcattg	gcgccgcaag	tacatcaaac	960
actttgttgc	actcgctgcg	ccatgggtg	ggacgatctc	tcagatgaag	acatttgctt	1020
ctggcaacac	actcgggtgc	ccttttagtta	accctttgct	ggtcagacgg	catcagagga	1080
cctccgagag	taaccaatgg	ctacttccat	ctaccaaagt	gtttcacgac	agaactaaac	1140
cgcttgctgt	aactccccag	gttaactaca	cagcttacga	gatggatcgg	ttttttgcag	1200
acattggatt	ctcacaagga	gttgtgcctt	acaagacaag	agtgttgctt	ttaacagagg	1260
agctgatgac	tcggggagtg	ccagtcactt	gcataatg	gagaggagtt	gatacaccgg	1320
aggttttgat	gtatggaaaa	ggaggattcg	ataagcaacc	agagattaag	tatggagatg	1380
gagatgggac	ggttaatttg	gcgagcttag	cagctttgaa	agtcgatagc	ttgaacaccg	1440
tagagattga	tggagtttgc	catacatcta	tacttaaaga	cgagatcgca	cttaaagaga	1500
ttatgaagca	gatttcaatt	attaattatg	aatttagcaa	tgtaaatgcc	gtcaatgaat	1560
ga						1562

<210> 11

<211> 3896

<212> DNA

<213> Arabidopsis thaliana

<400> 11

atgggagcga	attcgaaatc	agtaacggct	tccttcaccg	tcacgcgcgt	ttttttcttg	60
atttgcggtg	gccgaactgc	ggtggaggat	gagaccgagt	ttcacggcga	ctactcgaag	120
ctatcgggta	taatcattcc	gggatttgcg	tcgacgcagc	tacgagcgtg	gtcgatcctt	180
gactgtccat	acactccggt	ggacttcaat	ccgctcgacc	tcgtatggct	agacaccact	240
aaggtccggt	atcttcattt	ccttcgctcc	ttattctgtc	ggtcgagtca	cttggtgatg	300
aattccaagc	gaaatatagc	aatgaagcat	gtctcgtctc	tcttattgat	tcggttcatta	360
gtcaacagtg	acgcttctga	atctgagttt	agagtcatat	aaaacagctg	actcggcgag	420
tgtttcccat	cgcttttggt	tcgctaaatg	tagcgcaatg	aatgtgtaat	tagtctgcgc	480
tttttattca	actagatctg	caagtttttc	agagtgtca	atagtagtta	gaaaatgtta	540
ggtcatttta	cttggtgcatt	gtgattcttt	tggttggtgc	ttactgatcg	acgtgatgga	600
tggtttacag	cttctttctg	ctgtcaactg	ctggtttaag	tgatgggtgc	tagatcctta	660
taatcaaaca	gaccatcccc	agtgtaaagc	acggcctgac	agtggtcctt	cagccatcac	720
agaattggat	ccaggttaca	taacaggtag	tttcggattt	ttctttcttt	tgagttttct	780
tcaatttgat	atcatcttgt	tgtgatataa	tatggctaag	ttcattaatt	tggtcaattt	840
tcaggctctc	tttctactgt	ctggaaagag	tggcttaagt	gggtgtgtga	gtttgggtata	900
gaagcaaatg	caattgtcgc	tgttccatac	gattggagat	tgtaaccaac	caaattggaa	960
gagcgtgacc	tttactttca	caagctcaag	ttagtcttta	tcaggctaat	gtctttttatc	1020
ttctcttttt	atgtaagata	agctaagagc	tctggctcgtc	ttcctttttg	cagggttgacc	1080
tttgaaactg	ctttaaaact	ccgtggcggc	ccttctatag	tatttgacca	ttcaatgggt	1140
aataatgtct	tcagatactt	tctggaatgg	ctgaggctag	aaattgcacc	aaaacattat	1200
ttgaagtggc	ttgatcagca	tatccatgct	tatttctgctg	ttggtaccgg	cctactatcc	1260
ttaagtttacc	attttatttt	ttctctaatt	gggggagtta	tggtgtgact	tactggattg	1320
agctcgatac	ctgatttgggt	gttgatttag	gagctcctct	tcttggttct	gttgaggcaa	1380
tcaaactctac	tctctctggt	gtaacgtttg	gccttctctg	ttctgaggtg	acctctgact	1440

C1
Cont

tctcttttagt ttttaagtagt tgatatcaac caggtcttat aactcactgg attttccttt 1500
tgaaagtatt acttttggtta attgaactgc tgtacgcgat atggatatctg tagatcttga 1560
agtgctagtt atcaaagaac atatttggtg tagtatacct gtcagcggcc ttagctaata 1620
caaccaaacc acatgtacac tgatttagtt ttcagattat tatggtagac ttttaagttga 1680
gaagaaactt tgactgaaat ctcttttatt taataggcta tgatttggtt attgaaatca 1740
tgtgacatat tgacatgcgc ttctcatggt ttttggtggc aaggcttcag ggaactgctc 1800
ggttggtgtc caattctttt gcgtcgtcat tgtggcttat gccattttca aagaattgca 1860
agggtgataa cacattctgg acgcattttt ctgggggtgc tgcaaagaaa gataagcgcg 1920
tataccactg tgatgaagag gaatatcaat caaaatatc tggctggccg acaaattata 1980
ttaacattga aattccttcc actagecgtt agactctgta tatgcaactg taacactaac 2040
aaaagtttca ccaagaatgt tcaactctcat atttcggtcc tttgatgtgt atccatcagt 2100
tacagaaaca gctctagtca acatgaccag catggaatgt ggccttccca cccttttgtc 2160
tttcacagcc cgtgaactag cagatgggac tcttttcaaa gcaatagaag actatgaccc 2220
agatagcaag aggatgttac accagtttaa gaagtacgta cctttctttg tgataagaaa 2280
tattgctcat cgatcatcac ttgctggctt cttgtacgtc aaattgtttt gtttaaactc 2340
ctatatcaat tgttcatatg ctttgtcttt cttactataa gaaacaagta taatcagaaa 2400
ccttattatt gattatcagt tctctcctta tattatggaa tgtctttttc gtttacagtt 2460
atgaatgcaa aagggggtat tttagttgat tgattctctc attctctagt ttgttttgac 2520
taatagcgtc aattttgttt ttctagcaaa tctttgtgaa ttatatataa catgctaact 2580
atacttttca ggttgatca tgatgaccct gtttttaatc ctctgactcc ttgggagaga 2640
ccacctataa aaaatgtatt ttgcatatat ggtgctcatc taaagacaga ggtatgatgc 2700
attctcaata tcacattatg cgttgacttt gttattatat tccccatttg gtttgcaata 2760
tctttttgaa ttatgattta tcttctcctt tgcactctat gctattaagc gttaaaggta 2820
ctaaatgtat gaagctgtct gtcatagggt ggttattact ttgccccaa gggcaaacct 2880
tattcctgata attggatcat cacggatata atttatgaaa ctgaagggtc cctcgtgtca 2940
aggtaatttt ccgcaatggc agaagtaaaa caggaaggca aagtcctctg tatcagtcta 3000
gtggcatgtt atctcagttg cataagcaaa ttattaaaca actaaaattt aagtactttt 3060
ttatcattcc ttttgagctt agtggatgat cagtggttta aagtgggaag aggtgttgca 3120
tgaaacatga cacttgatc aaagataact agcaaaacaa aactaaccca tttctgaatt 3180
tcatattatt aggagtagtc gtgcttttaa aaaatttgtt ttaagaaacc gaaaaactag 3240
ttcatactct gattgtgcaa tatctgcagg tctggaactg tggttgatgg gaacgctgga 3300
cctataactg gggatgagac ggtaaagctca gaagtgtgtt ttgaaattat cttcttgcaa 3360
actactgaag actaagataa tacttgcttc tgggaactg cttgctatgt tctctagtac 3420
actgcaatat tgactctccg ctacttttat tgattatgaa attgatctct tataggtacc 3480
ctatcattca ctctcttggg gcaagaattg gctcggactt aaagttaaca taacaatggc 3540
tccccaggta ctctttttta gttcctcacc ttatatagat caaactttaa gtgtactttt 3600
ctggttatgt gttgatttac ctccaatttg ttctttctaa aaatcatata tctctgtact 3660
cctcaagaac ttgtattaat ctaaaacgaga ttctcattgg gaaaataaaa caacagccag 3720
aacacgatgg aagcgacgta catgtggaac taaatgttga tcatgagcat gggtcagaca 3780
tcatagctaa catgacaaaa gcaccaaggg ttaagtacat aaccttttat gaagactctg 3840
agagcattcc ggggaagaga accgcagctc gggagcttga taaaagtggg tattaa 3896

<210> 12

<211> 709

<212> DNA

<213> *Lycopersicon esculentum*

<400> 12

ctggggccaa aagtgaacat aacaaggaca ccacagtcag agcatgatgt tcagatgtac 60
aagtgcattc aaatatagag catcaacatg gtgaagatat cattcccaat atgacaaagt 120
tacctacaat gaagtacata acctattatg aggattctga aagttttcca gggacaagaa 180
cagcagtttg ggagcttgat aaagcaaatc acaggaacat tgtcagatct ccagctttga 240
tgcgggagct gtggcttgag atgtggcatg atattcatcc tgataaaaag tccaagtttg 300
ttacaaaagg tgggtgtctga tctcactat tttcttctat aaatgtttga gtttgtattg 360
actattgaag tattgaaca aaaagcaaa cgtgggctc tgagggatga ggactgctat 420
tgggattacg ggaagctcgt atgtgcatgg gctgaacatt gtgaatacag gttagaatat 480
tcaaattata ttttgcaaaa tattctcttt ttgtgtattt aggccacctt tccccggtca 540

C1
Cont

caacgatgca gatatgtatt cgggatgtt cacctgggac agagttgcag attgaagagt 600
 tctacatctc acatcctgtc acactatgtg tgatatttaa gaaactttgt ttggcggaa 660
 aacaagtttg cacaacatt tgaagaagaa agcgaaatga ttcagagag 709

<210> 13
 <211> 623
 <212> PRT
 <213> Schizosaccharomyces pombe

<400> 13

Met Ala Ser Ser Lys Lys Ser Lys Thr His Lys Lys Lys Lys Glu Val
 1 5 10 15
 Lys Ser Pro Ile Asp Leu Pro Asn Ser Lys Lys Pro Thr Arg Ala Leu
 20 25 30
 Ser Glu Gln Pro Ser Ala Ser Glu Thr Gln Ser Val Ser Asn Lys Ser
 35 40 45
 Arg Lys Ser Lys Phe Gly Lys Arg Leu Asn Phe Ile Leu Gly Ala Ile
 50 55 60
 Leu Gly Ile Cys Gly Ala Phe Phe Phe Ala Val Gly Asp Asp Asn Ala
 65 70 75 80
 Val Phe Asp Pro Ala Thr Leu Asp Lys Phe Gly Asn Met Leu Gly Ser
 85 90 95
 Ser Asp Leu Phe Asp Asp Ile Lys Gly Tyr Leu Ser Tyr Asn Val Phe
 100 105 110
 Lys Asp Ala Pro Phe Thr Thr Asp Lys Pro Ser Gln Ser Pro Ser Gly
 115 120 125
 Asn Glu Val Gln Val Gly Leu Asp Met Tyr Asn Glu Gly Tyr Arg Ser
 130 135 140
 Asp His Pro Val Ile Met Val Pro Gly Val Ile Ser Ser Gly Leu Glu
 145 150 155 160
 Ser Trp Ser Phe Asn Asn Cys Ser Ile Pro Tyr Phe Arg Lys Arg Leu
 165 170 175
 Trp Gly Ser Trp Ser Met Leu Lys Ala Met Phe Leu Asp Lys Gln Cys
 180 185 190
 Trp Leu Glu His Leu Met Leu Asp Lys Lys Thr Gly Leu Asp Pro Lys
 195 200 205
 Gly Ile Lys Leu Arg Ala Ala Gln Gly Phe Glu Ala Ala Asp Phe Phe
 210 215 220
 Ile Thr Gly Tyr Trp Ile Trp Ser Lys Val Ile Glu Asn Leu Ala Ala
 225 230 235 240
 Ile Gly Tyr Glu Pro Asn Asn Met Leu Ser Ala Ser Tyr Asp Trp Arg
 245 250 255

C1
 Cont

Leu Ser Tyr Ala Asn Leu Glu Glu Arg Asp Lys Tyr Phe Ser Lys Leu
 260 265 270
 Lys Met Phe Ile Glu Tyr Ser Asn Ile Val His Lys Lys Lys Val Val
 275 280 285
 Leu Ile Ser His Ser Met Gly Ser Gln Val Thr Tyr Tyr Phe Phe Lys
 290 295 300
 Trp Val Glu Ala Glu Gly Tyr Gly Asn Gly Gly Pro Thr Trp Val Asn
 305 310 315 320
 Asp His Ile Glu Ala Phe Ile Asn Ile Ser Gly Ser Leu Ile Gly Ala
 325 330 335
 Pro Lys Thr Val Ala Ala Leu Leu Ser Gly Glu Met Lys Asp Thr Gly
 340 345 350
 Ile Val Ile Thr Leu Asn Ile Leu Glu Lys Phe Phe Ser Arg Ser Glu
 355 360 365
 Arg Ala Met Met Val Arg Thr Met Gly Gly Val Ser Ser Met Leu Pro
 370 375 380
 Lys Gly Gly Asp Val Ala Pro Asp Asp Leu Asn Gln Thr Asn Phe Ser
 385 390 395 400
 Asn Gly Ala Ile Ile Arg Tyr Arg Glu Asp Ile Asp Lys Asp His Asp
 405 410 415
 Glu Phe Asp Ile Asp Asp Ala Leu Gln Phe Leu Lys Asn Val Thr Asp
 420 425 430
 Asp Asp Phe Lys Val Met Leu Ala Lys Asn Tyr Ser His Gly Leu Ala
 435 440 445
 Trp Thr Glu Lys Glu Val Leu Lys Asn Asn Glu Met Pro Ser Lys Trp
 450 455 460
 Ile Asn Pro Leu Glu Thr Ser Leu Pro Tyr Ala Pro Asp Met Lys Ile
 465 470 475 480
 Tyr Cys Val His Gly Val Gly Lys Pro Thr Glu Arg Gly Tyr Tyr Tyr
 485 490 495
 Thr Asn Asn Pro Glu Gly Gln Pro Val Ile Asp Ser Ser Val Asn Asp
 500 505 510
 Gly Thr Lys Val Glu Asn Gly Ile Val Met Asp Asp Gly Asp Gly Thr
 515 520 525
 Leu Pro Ile Leu Ala Leu Gly Leu Val Cys Asn Lys Val Trp Gln Thr
 530 535 540
 Lys Arg Phe Asn Pro Ala Asn Thr Ser Ile Thr Asn Tyr Glu Ile Lys
 545 550 555 560
 His Glu Pro Ala Ala Phe Asp Leu Arg Gly Gly Pro Arg Ser Ala Glu
 565 570 575

C1
 Cont

His Val Asp Ile Leu Gly His Ser Glu Leu Asn Glu Ile Ile Leu Lys
580 585 590

Val Ser Ser Gly His Gly Asp Ser Val Pro Asn Arg Tyr Ile Ser Asp
595 600 605

Ile Gln Glu Ile Ile Asn Glu Ile Asn Leu Asp Lys Pro Arg Asn
610 615 620

<210> 14

<211> 432

<212> PRT

<213> Arabidopsis thaliana

<400> 14

Met Lys Lys Ile Ser Ser His Tyr Ser Val Val Ile Ala Ile Leu Val
1 5 10 15

Val Val Thr Met Thr Ser Met Cys Gln Ala Val Gly Ser Asn Val Tyr
20 25 30

Pro Leu Ile Leu Val Pro Gly Asn Gly Gly Asn Gln Leu Glu Val Arg
35 40 45

Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val Trp Cys Ser Ser Trp Leu
50 55 60

Tyr Pro Ile His Lys Lys Ser Gly Gly Trp Phe Arg Leu Trp Phe Asp
65 70 75 80

Ala Ala Val Leu Leu Ser Pro Phe Thr Arg Cys Phe Ser Asp Arg Met
85 90 95

Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp Tyr Gln Asn Ala Pro Gly
100 105 110

Val Gln Thr Arg Val Pro His Phe Gly Ser Thr Lys Ser Leu Leu Tyr
115 120 125

Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser Tyr Met Glu His Leu Val
130 135 140

Lys Ala Leu Glu Lys Lys Cys Gly Tyr Val Asn Asp Gln Thr Ile Leu
145 150 155 160

Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu Ala Ala Ser Gly His Pro
165 170 175

Ser Arg Val Ala Ser Gln Phe Leu Gln Asp Leu Lys Gln Leu Val Glu
180 185 190

Lys Thr Ser Ser Glu Asn Glu Gly Lys Pro Val Ile Leu Leu Ser His
195 200 205

Ser Leu Gly Gly Leu Phe Val Leu His Phe Leu Asn Arg Thr Thr Pro
210 215 220

C1
Cont

Ser Trp Arg Arg Lys Tyr Ile Lys His Phe Val Ala Leu Ala Ala Pro
 225 230 235 240
 Trp Gly Gly Thr Ile Ser Gln Met Lys Thr Phe Ala Ser Gly Asn Thr
 245 250 255
 Leu Gly Val Pro Leu Val Asn Pro Leu Leu Val Arg Arg His Gln Arg
 260 265 270
 Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro Ser Thr Lys Val Phe His
 275 280 285
 Asp Arg Thr Lys Pro Leu Val Val Thr Pro Gln Val Asn Tyr Thr Ala
 290 295 300
 Tyr Glu Met Asp Arg Phe Phe Ala Asp Ile Gly Phe Ser Gln Gly Val
 305 310 315 320
 Val Pro Tyr Lys Thr Arg Val Leu Pro Leu Thr Glu Glu Leu Met Thr
 325 330 335
 Pro Gly Val Pro Val Thr Cys Ile Tyr Gly Arg Gly Val Asp Thr Pro
 340 345 350
 Glu Val Leu Met Tyr Gly Lys Gly Gly Phe Asp Lys Gln Pro Glu Ile
 355 360 365
 Lys Tyr Gly Asp Gly Asp Gly Thr Val Asn Leu Ala Ser Leu Ala Ala
 370 375 380
 Leu Lys Val Asp Ser Leu Asn Thr Val Glu Ile Asp Gly Val Ser His
 385 390 395 400
 Thr Ser Ile Leu Lys Asp Glu Ile Ala Leu Lys Glu Ile Met Lys Gln
 405 410 415
 Ile Ser Ile Ile Asn Tyr Glu Leu Ala Asn Val Asn Ala Val Asn Glu
 420 425 430

<210> 15
 <211> 552
 <212> PRT
 <213> Arabidopsis thaliana

<400> 15

Met Gly Ala Asn Ser Lys Ser Val Thr Ala Ser Phe Thr Val Ile Ala
 1 5 10 15
 Val Phe Phe Leu Ile Cys Gly Gly Arg Thr Ala Val Glu Asp Glu Thr
 20 25 30
 Glu Phe His Gly Asp Tyr Ser Lys Leu Ser Gly Ile Ile Ile Pro Gly
 35 40 45

C1
Cont

Phe Ala Ser Thr Gln Leu Arg Ala Trp Ser Ile Leu Asp Cys Pro Tyr
 50 55 60
 Thr Pro Leu Asp Phe Asn Pro Leu Asp Leu Val Trp Leu Asp Thr Thr
 65 70 75 80
 Lys Leu Leu Ser Ala Val Asn Cys Trp Phe Lys Cys Met Val Leu Asp
 85 90 95
 Pro Tyr Asn Gln Thr Asp His Pro Glu Cys Lys Ser Arg Pro Asp Ser
 100 105 110
 Gly Leu Ser Ala Ile Thr Glu Leu Asp Pro Gly Tyr Ile Thr Gly Pro
 115 120 125
 Leu Ser Thr Val Trp Lys Glu Trp Leu Lys Trp Cys Val Glu Phe Gly
 130 135 140
 Ile Glu Ala Asn Ala Ile Val Ala Val Pro Tyr Asp Trp Arg Leu Ser
 145 150 155 160
 Pro Thr Lys Leu Glu Glu Arg Asp Leu Tyr Phe His Lys Leu Lys Leu
 165 170 175
 Thr Phe Glu Thr Ala Leu Lys Leu Arg Gly Gly Pro Ser Ile Val Phe
 180 185 190
 Ala His Ser Met Gly Asn Asn Val Phe Arg Tyr Phe Leu Glu Trp Leu
 195 200 205
 Arg Leu Glu Ile Ala Pro Lys His Tyr Leu Lys Trp Leu Asp Gln His
 210 215 220
 Ile His Ala Tyr Phe Ala Val Gly Ala Pro Leu Leu Gly Ser Val Glu
 225 230 235 240
 Ala Ile Lys Ser Thr Leu Ser Gly Val Thr Phe Gly Leu Pro Val Ser
 245 250 255
 Glu Gly Thr Ala Arg Leu Leu Ser Asn Ser Phe Ala Ser Ser Leu Trp
 260 265 270
 Leu Met Pro Phe Ser Lys Asn Cys Lys Gly Asp Asn Thr Phe Trp Thr
 275 280 285
 His Phe Ser Gly Gly Ala Ala Lys Lys Asp Lys Arg Val Tyr His Cys
 290 295 300
 Asp Glu Glu Glu Tyr Gln Ser Lys Tyr Ser Gly Trp Pro Thr Asn Ile
 305 310 315 320
 Ile Asn Ile Glu Ile Pro Ser Thr Ser Ala Arg Glu Leu Ala Asp Gly
 325 330 335
 Thr Leu Phe Lys Ala Ile Glu Asp Tyr Asp Pro Asp Ser Lys Arg Met
 340 345 350
 Leu His Gln Leu Lys Lys Tyr Val Pro Phe Phe Val Ile Arg Asn Ile
 355 360 365

C1
 Cont

Ala His Arg Ser Ser Leu Ala Gly Phe Leu Leu Tyr His Asp Asp Pro
 370 375 380

Val Phe Asn Pro Leu Thr Pro Trp Glu Arg Pro Pro Ile Lys Asn Val
 385 390 395 400

Phe Cys Ile Tyr Gly Ala His Leu Lys Thr Glu Val Gly Tyr Tyr Phe
 405 410 415

Ala Pro Ser Gly Lys Pro Tyr Pro Asp Asn Trp Ile Ile Thr Asp Ile
 420 425 430

Ile Tyr Glu Thr Glu Gly Ser Leu Val Ser Arg Ser Gly Thr Val Val
 435 440 445

Asp Gly Asn Ala Gly Pro Ile Thr Gly Asp Glu Thr Val Pro Tyr His
 450 455 460

Ser Leu Ser Trp Cys Lys Asn Trp Leu Gly Pro Lys Val Asn Ile Thr
 465 470 475 480

Met Ala Pro Gln Ile Leu Ile Gly Lys Ile Lys Gln Gln Pro Glu His
 485 490 495

Asp Gly Ser Asp Val His Val Glu Leu Asn Val Asp His Glu His Gly
 500 505 510

Ser Asp Ile Ile Ala Asn Met Thr Lys Ala Pro Arg Val Lys Tyr Ile
 515 520 525

Thr Phe Tyr Glu Asp Ser Glu Ser Ile Pro Gly Lys Arg Thr Ala Val
 530 535 540

Trp Glu Leu Asp Lys Ser Gly Tyr
 545 550

<210> 1a
 <211> 661
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 1a

Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
 1 5 10 15

Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 20 25 30

Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 35 40 45

Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 50 55 60

Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
 65 70 75 80

Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
 85 90 95
 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
 100 105 110
 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
 115 120 125
 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
 130 135 140
 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
 145 150 155 160
 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
 165 170 175
 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
 180 185 190
 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
 195 200 205
 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
 210 215 220
 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
 225 230 235 240
 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
 245 250 255
 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
 260 265 270
 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
 275 280 285
 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
 290 295 300
 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
 305 310 315 320
 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
 325 330 335
 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
 340 345 350
 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
 355 360 365
 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
 370 375 380
 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
 385 390 395 400

C1
 Cont

Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
 405 410 415
 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
 420 425 430
 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
 435 440 445
 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
 450 455 460
 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
 465 470 475 480
 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
 485 490 495
 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
 500 505 510
 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
 515 520 525
 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
 530 535 540
 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
 545 550 555 560
 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575
 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
 580 585 590
 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
 595 600 605
 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
 610 615 620
 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
 625 630 635 640
 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 645 650 655
 Met Pro Phe Pro Met
 660

<210> 2a
 <211> 387
 <212> PRT
 <213> Arabidopsis thaliana

<400> 2a

C1
Cont

Val Gly Ser Asn Val Tyr Pro Leu Ile Leu Val Pro Gly Asn Gly Gly
 1 5 10 15
 Asn Gln Leu Glu Val Arg Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val
 20 25 30
 Trp Cys Ser Ser Trp Leu Tyr Pro Ile His Lys Lys Ser Gly Gly Trp
 35 40 45
 Phe Arg Leu Trp Phe Asp Ala Ala Val Leu Leu Ser Pro Phe Thr Arg
 50 55 60
 Cys Phe Ser Asp Arg Met Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp
 65 70 75 80
 Tyr Gln Asn Ala Pro Gly Val Gln Thr Arg Val Pro His Phe Gly Ser
 85 90 95
 Thr Lys Ser Leu Leu Tyr Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser
 100 105 110
 Tyr Met Glu His Leu Val Lys Ala Leu Glu Lys Lys Cys Gly Tyr Val
 115 120 125
 Asn Asp Gln Thr Ile Leu Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu
 130 135 140
 Ala Ala Ser Gly His Pro Ser Arg Val Ala Ser Gln Phe Leu Gln Asp
 145 150 155 160
 Leu Lys Gln Leu Val Glu Lys Thr Ser Ser Glu Asn Glu Gly Lys Pro
 165 170 175
 Val Ile Leu Leu Ser His Ser Leu Gly Gly Leu Phe Val Leu His Phe
 180 185 190
 Leu Asn Arg Thr Thr Pro Ser Trp Arg Arg Lys Tyr Ile Lys His Phe
 195 200 205
 Val Ala Leu Ala Ala Pro Trp Gly Gly Thr Ile Ser Gln Met Lys Thr
 210 215 220
 Phe Ala Ser Gly Asn Thr Leu Gly Val Pro Leu Val Asn Pro Leu Leu
 225 230 235 240
 Val Arg Arg His Gln Arg Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro
 245 250 255
 Ser Thr Lys Val Phe His Asp Arg Thr Lys Pro Leu Val Val Thr Pro
 260 265 270
 Gln Val Asn Tyr Thr Ala Tyr Glu Met Asp Arg Phe Phe Ala Asp Ile
 275 280 285
 Gly Phe Ser Gln Gly Val Val Pro Tyr Lys Thr Arg Val Leu Pro Leu
 290 295 300
 Thr Glu Glu Leu Met Thr Pro Gly Val Pro Val Thr Cys Ile Tyr Gly
 305 310 315 320

C1
 Cont

Arg Gly Val Asp Thr Pro Glu Val Leu Met Tyr Gly Lys Gly Gly Phe
325 330 335

Asp Lys Gln Pro Glu Ile Lys Tyr Gly Asp Gly Asp Gly Thr Val Asn
340 345 350

Leu Ala Ser Leu Ala Ala Leu Lys Val Asp Ser Leu Asn Thr Val Glu
355 360 365

Ile Asp Gly Val Ser His Thr Ser Ile Leu Lys Asp Glu Ile Ala Leu
370 375 380

Lys Glu Ile
385

<210> 3a

<211> 389

<212> PRT

<213> Arabidopsis thaliana

<400> 3a

Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe Ile Pro
1 5 10 15

Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln Cys Ala
20 25 30

Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Leu Cys Trp
35 40 45

Val Glu His Met Ser Leu Asp Asn Glu Thr Gly Leu Asp Pro Ala Gly
50 55 60

Ile Arg Val Arg Ala Val Ser Gly Leu Val Ala Ala Asp Tyr Phe Ala
65 70 75 80

Pro Gly Tyr Phe Val Trp Ala Val Leu Ile Ala Asn Leu Ala His Ile
85 90 95

Gly Tyr Glu Glu Lys Asn Met Tyr Met Ala Ala Tyr Asp Trp Arg Leu
100 105 110

Ser Phe Gln Asn Thr Glu Arg Asp Gln Thr Leu Ser Arg Met Lys Ser
115 120 125

Asn Ile Glu Leu Met Val Ser Thr Asn Gly Gly Lys Lys Ala Val Ile
130 135 140

Val Pro His Ser Met Gly Val Leu Tyr Phe Leu His Phe Met Lys Trp
145 150 155 160

Val Glu Ala Pro Ala Pro Leu Gly Gly Gly Gly Pro Asp Trp Cys
165 170 175

Ala Lys Tyr Ile Lys Ala Val Met Asn Ile Gly Gly Pro Phe Leu Gly
180 185 190

Cl
Cont

Val Pro Lys Ala Val Ala Gly Leu Phe Ser Ala Glu Ala Lys Asp Met
 195 200 205
 Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu Pro Lys Gly
 210 215 220
 Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu Leu Pro Asn
 225 230 235 240
 Ala Pro Glu Met Glu Ile Tyr Ser Leu Tyr Gly Val Gly Ile Pro Thr
 245 250 255
 Glu Arg Ala Tyr Val Tyr Lys Leu Asn Gln Ser Pro Asp Ser Cys Ile
 260 265 270
 Pro Phe Gln Ile Phe Thr Ser Ala His Glu Glu Asp Glu Asp Ser Cys
 275 280 285
 Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val Pro Val
 290 295 300
 Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys Thr Arg
 305 310 315 320
 Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn His Ser
 325 330 335
 Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly Ala His
 340 345 350
 Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met Arg Val
 355 360 365
 Ala Ala Gly Gly Asn Gly Ser Asp Ile Gly His Asp Gln Val His Ser
 370 375 380
 Gly Ile Phe Glu Trp
 385

C1
 cont
 <210> 4a
 <211> 1986
 <212> DNA
 <213> Saccharomyces cerevisiae

<220>
 <221> CDS
 <222> (1) .. (1983)

<400> 4a

atg ggc aca ctg ttt cga aga aat gtc cag aac caa aag agt gat tct 48
 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
 1 5 10 15
 gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga 96
 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 20 25 30

aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt 144
 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 35 40 45

att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg 192
 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 50 55 60

aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg 240
 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
 65 70 75 80

att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt 288
 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
 85 90 95

ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt 336
 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
 100 105 110

gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt 384
 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
 115 120 125

ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac 432
 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
 130 135 140

tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt 480
 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
 145 150 155 160

aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta 528
 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
 165 170 175

atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att 576
 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
 180 185 190

gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg 624
 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
 195 200 205

gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg 672
 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
 210 215 220

ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac 720
 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
 225 230 235 240

ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc 768
 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
 245 250 255

gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att 816
 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
 260 265 270

C1
 Cont

ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt 864
 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
 275 280 285

gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag 912
 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
 290 295 300

gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta 960
 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
 305 310 315 320

att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg 1008
 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
 325 330 335

gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt 1056
 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
 340 345 350

aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc 1104
 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
 355 360 365

gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc 1152
 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
 370 375 380

att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca 1200
 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
 385 390 395 400

aga att gag aga gta aaa atg tta caa acg tgg ggt ggt ata cca tca 1248
 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
 405 410 415

atg cta cca aag gga gaa gag gtc att tgg ggg gat atg aag tca tct 1296
 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
 420 425 430

tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att 1344
 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
 435 440 445

cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg 1392
 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
 450 455 460

aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa 1440
 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
 465 470 475 480

aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa 1488
 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
 485 490 495

gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg 1536
 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
 500 505 510

C1
 Cont

gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac 1584
 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
 515 520 525

ggg gtg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat 1632
 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
 530 535 540

gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag caa cct 1680
 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
 545 550 555 560

gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca 1728
 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575

atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga 1776
 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
 580 585 590

att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat 1824
 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
 595 600 605

ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc 1872
 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
 610 615 620

gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat 1920
 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
 625 630 635 640

ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag 1968
 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 645 650 655

atg ccc ttc cca atg taa 1986
 Met Pro Phe Pro Met
 660

<210> 5a
 <211> 661
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 5a

Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
 1 5 10 15

Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 20 25 30

Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 35 40 45

Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 50 55 60

C1
 Cont

Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
 65 70 75 80
 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
 85 90 95
 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
 100 105 110
 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
 115 120 125
 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
 130 135 140
 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
 145 150 155 160
 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
 165 170 175
 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
 180 185 190
 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
 195 200 205
 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
 210 215 220
 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
 225 230 235 240
 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
 245 250 255
 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
 260 265 270
 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
 275 280 285
 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
 290 295 300
 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
 305 310 315 320
 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
 325 330 335
 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
 340 345 350
 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
 355 360 365
 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
 370 375 380

C1
 Cont.

Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
 385 390 395 400
 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
 405 410 415
 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
 420 425 430
 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
 435 440 445
 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
 450 455 460
 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
 465 470 475 480
 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
 485 490 495
 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
 500 505 510
 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
 515 520 525
 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
 530 535 540
 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
 545 550 555 560
 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575
 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
 580 585 590
 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
 595 600 605
 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
 610 615 620
 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
 625 630 635 640
 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 645 650 655
 Met Pro Phe Pro Met
 660

<210> 1b
 <211> 1986
 <212> DNA
 <213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> (1)..(1983)

<400> 1b

atg ggc aca ctg ttt cga aga aat gtc cag aac caa aag agt gat tct 48
 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
 1 5 10 15

gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga 96
 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 20 25 30

aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt 144
 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 35 40 45

att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg 192
 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 50 55 60

aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg 240
 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
 65 70 75 80

att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt 288
 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
 85 90 95

ggc gct tat cat gtt cat aat agc gat ago gac ttg ttt gac aac ttt 336
 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
 100 105 110

gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt 384
 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
 115 120 125

ctc cca caa ggt ata agt tgc ttt att gat gat att cag gct ggt aac 432
 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
 130 135 140

tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt 480
 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
 145 150 155 160

aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta 528
 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
 165 170 175

atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att 576
 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
 180 185 190

gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg 624
 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
 195 200 205

gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg 672

C1
Cont

Gly	Ser	Phe	Tyr	Met	Leu	Arg	Thr	Met	Val	Met	Asp	Lys	Val	Cys	Trp	
210						215					220					
ttg	aaa	cat	gta	atg	tta	gat	cct	gaa	aca	ggg	ctg	gac	cca	ccg	aac	720
Leu	Lys	His	Val	Met	Leu	Asp	Pro	Glu	Thr	Gly	Leu	Asp	Pro	Pro	Asn	
225					230					235					240	
ttt	acg	cta	cgt	gca	gca	cag	ggc	ttc	gaa	tca	act	gat	tat	ttc	atc	768
Phe	Thr	Leu	Arg	Ala	Ala	Gln	Gly	Phe	Glu	Ser	Thr	Asp	Tyr	Phe	Ile	
				245					250					255		
gca	ggg	tat	tgg	att	tgg	aac	aaa	gtt	ttc	caa	aat	ctg	gga	gta	att	816
Ala	Gly	Tyr	Trp	Ile	Trp	Asn	Lys	Val	Phe	Gln	Asn	Leu	Gly	Val	Ile	
			260					265					270			
ggc	tat	gaa	ccc	aat	aaa	atg	acg	agt	gct	gcg	tat	gat	tgg	agg	ctt	864
Gly	Tyr	Glu	Pro	Asn	Lys	Met	Thr	Ser	Ala	Ala	Tyr	Asp	Trp	Arg	Leu	
	275						280					285				
gca	tat	tta	gat	cta	gaa	aga	cgc	gat	agg	tac	ttt	acg	aag	cta	aag	912
Ala	Tyr	Leu	Asp	Leu	Glu	Arg	Arg	Asp	Arg	Tyr	Phe	Thr	Lys	Leu	Lys	
	290					295					300					
gaa	caa	atc	gaa	ctg	ttt	cat	caa	ttg	agt	ggg	gaa	aaa	gtt	tgt	tta	960
Glu	Gln	Ile	Glu	Leu	Phe	His	Gln	Leu	Ser	Gly	Glu	Lys	Val	Cys	Leu	
305					310					315					320	
att	gga	cat	tct	atg	ggg	tct	cag	att	atc	ttt	tac	ttt	atg	aaa	tgg	1008
Ile	Gly	His	Ser	Met	Gly	Ser	Gln	Ile	Ile	Phe	Tyr	Phe	Met	Lys	Trp	
				325					330					335		
gtc	gag	gct	gaa	ggc	cct	ctt	tac	ggg	aat	ggg	ggg	cgt	ggc	tgg	gtt	1056
Val	Glu	Ala	Glu	Gly	Pro	Leu	Tyr	Gly	Asn	Gly	Gly	Arg	Gly	Trp	Val	
			340					345					350			
aac	gaa	cac	ata	gat	tca	ttc	att	aat	gca	gca	ggg	acg	ctt	ctg	ggc	1104
Asn	Glu	His	Ile	Asp	Ser	Phe	Ile	Asn	Ala	Ala	Gly	Thr	Leu	Leu	Gly	
		355					360					365				
gct	cca	aag	gca	gtt	cca	gct	cta	att	agt	ggg	gaa	atg	aaa	gat	acc	1152
Ala	Pro	Lys	Ala	Val	Pro	Ala	Leu	Ile	Ser	Gly	Glu	Met	Lys	Asp	Thr	
	370					375					380					
att	caa	tta	aat	acg	tta	gcc	atg	tat	ggg	ttg	gaa	aag	ttc	ttc	tca	1200
Ile	Gln	Leu	Asn	Thr	Leu	Ala	Met	Tyr	Gly	Leu	Glu	Lys	Phe	Phe	Ser	
385					390					395					400	
aga	att	gag	aga	gta	aaa	atg	tta	caa	acg	tgg	ggg	ggg	ata	cca	tca	1248
Arg	Ile	Glu	Arg	Val	Lys	Met	Leu	Gln	Thr	Trp	Gly	Gly	Ile	Pro	Ser	
				405					410					415		
atg	cta	cca	aag	gga	gaa	gag	gtc	att	tgg	ggg	gat	atg	aag	tca	tct	1296
Met	Leu	Pro	Lys	Gly	Glu	Glu	Val	Ile	Trp	Gly	Asp	Met	Lys	Ser	Ser	
			420				425						430			
tca	gag	gat	gca	ttg	aat	aac	aac	act	gac	aca	tac	ggc	aat	ttc	att	1344
Ser	Glu	Asp	Ala	Leu	Asn	Asn	Asn	Thr	Asp	Thr	Tyr	Gly	Asn	Phe	Ile	
	435					440						445				

C1
Cont

cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg 1392
 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
 450 455 460

aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa 1440
 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
 465 470 475 480

aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa 1488
 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
 485 490 495

gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg 1536
 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
 500 505 510

gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac 1584
 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
 515 520 525

ggg gtg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat 1632
 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
 530 535 540

gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag caa cct 1680
 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
 545 550 555 560

gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca 1728
 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575

atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga 1776
 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
 580 585 590

att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat 1824
 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
 595 600 605

ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc 1872
 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
 610 615 620

gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat 1920
 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
 625 630 635 640

ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag 1968
 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 645 650 655

atg ccc ttc cca atg taa 1986
 Met Pro Phe Pro Met
 660

<210> 2b
 <211> 661

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 2b

Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
 1 5 10 15
 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 20 25 30
 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 35 40 45
 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 50 55 60
 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
 65 70 75 80
 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
 85 90 95
 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
 100 105 110
 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
 115 120 125
 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
 130 135 140
 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
 145 150 155 160
 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
 165 170 175
 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
 180 185 190
 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
 195 200 205
 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
 210 215 220
 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
 225 230 235 240
 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
 245 250 255
 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
 260 265 270
 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
 275 280 285

C1
 Cont

Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
 290 295 300
 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
 305 310 315 320
 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
 325 330 335
 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
 340 345 350
 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
 355 360 365
 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
 370 375 380
 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
 385 390 395 400
 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
 405 410 415
 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
 420 425 430
 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
 435 440 445
 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
 450 455 460
 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
 465 470 475 480
 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
 485 490 495
 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
 500 505 510
 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
 515 520 525
 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
 530 535 540
 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
 545 550 555 560
 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575
 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
 580 585 590
 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
 595 600 605

C1
 Cont

Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
610 615 620

Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
625 630 635 640

Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
645 650 655

Met Pro Phe Pro Met
660

<210> 3b
<211> 2312
<212> DNA
<213> Schizosaccharomyces pombe

<400> 3b

atggcgctctt ccaagaagag caaaactcat aagaaaaaga aagaagtcaa atctcctatc 60
gacttaccaa attcaaagaa accaactcgc gctttgagtg agcaaccttc agcgctccgaa 120
acacaatctg tttcaaataa atcaagaaaa tctaaatttg gaaaaagatt gaattttata 180
ttgggcgcta ttttggaat atgcggtgct tttttttcgt ctggtggaga cgacaatgct 240
gttttcgacc ctgctacgtt agataaattt gggaatatgc taggctcttc agacttggtt 300
gatgacatta aaggatatat atcttataat gtgtttaagg atgcaccttt tactacggac 360
aagccttcgc agtctcctag cggaaatgaa gttcaagttg gtcttgatat gtacaatgag 420
ggatatcgaa gtgaccatcc tgttattatg gttcctgggtg ttatcagctc aggattagaa 480
agttggctgt ttaataattg ctcgattcct tactttagga aacgtctttg gggtagctgg 540
tctatgctga aggcaatggt ccttgacaag caatgctggc ttgaacattt aatgcttgat 600
aaaaaaaccg gcttggatcc gaagggaatt aagctgctga cagctcaggg gtttgaagca 660
gctgattttt ttatcacggg ctattggatt tggagtaaa taattgaaaa ccttgctgca 720
attggttatg agcctaataa catgttaagt gcttcttacg attggcgggt atcatatgca 780
aatttagagg aacgtgataa atatttttca aagttaaaaa tgttcattga gtacagcaac 840
attgtacata agaaaaaggt agtgttgatt tctcactcca tgggttcaca gggtacgtac 900
tattttttta agtgggttga agctgagggc tacggaaatg gtggaccgac ttgggttaat 960
gatcatattg aagcatttat aaatgtgagt ctcgatgggt gtttgactac gtttctaact 1020
tttgaataga tatcgggatc tttgattgga gcacccaaaa cagtggcagc gcttttatcg 1080
ggtgaaatga aagatacagg tattgtaatt acattaaaca ttttaatat taatttttgc 1140
taaccgtttt aagctcaatt gaatcagttt tgggtctatg ggttaagcaat aaattgttga 1200
gatttggttac taatttactg tttagtttgg aaaaattttt tccccgttct gaggtatatt 1260
caaaaataca aatgtgctct actttttcta acttttaata gagagccatg atggttcgca 1320
ctatgggagg agttagtct atgcttccta aaggaggcga tgttgatgg ggaaatgcca 1380
gttgggtaag aaatatgtgc tgttaatttt ttattaatat ttaggctcca gatgatctta 1440
atcaaacaaa tttttccaat ggtgcaatta ttcgatatag agaagacatt gataaggacc 1500
acgatgaatt tgacatagat gatgcattac aattttttaa aaatgttaca gatgacgatt 1560
ttaaagtcac cttagcgaaa aattattccc acggctcttg ttggactgaa aaagaagtgt 1620
taaaaaataa cgaaatgccg tctaaatgga taaatccgct agaagtaaga acattaaagt 1680
tactaaatta tactaaccga aatagactag tcttccttat gctcctgata tgaaaattta 1740
ttgcgttcac ggggtcggaa aaccaactga gagaggttat tatttacta ataactctga 1800
ggggcaacct gtcattgatt cctcgggtta tgatggaaca aaagtggaaa atgtgagaga 1860
atztatgttt caaacattct attaaactgt ttattagggg attgttatgg atgatggtga 1920
tggaacttta ccaatattag cccttggttt ggtgtgcaat aaagttggc aaacaaaaag 1980
gtttaatcct gctaatacaa gtatcacaaa ttatgaaatc aagcatgaac ctgctgcgtt 2040
tgatctgaga ggaggacctc gctcggcaga acacgtcgat atacttgac attcagagct 2100
aaatgtatgt tcattttacc ttacaaattt ctattactaa ctcttgaaat aaggaaatta 2160
ttttaaaagt ttcacagggc catggtgact cggttacaaa ccgttatata tcagatatcc 2220

C1
Cons

agtacggaca taagttttgt agattgcaat taactaacta accgaacagg gaaataataa 2280
atgagataaa tctcgataaa cctagaatt aa 2312

<210> 4b

<211> 3685

<212> DNA

<213> Arabidopsis thaliana

<400> 4b

atgccccctta ttcacgga aaagccgacg gagaaacat cgacgccgcc atctgaagag 60
gtggtgcacg atgaggattc gcaaaagaaa ccacacgaat cttccaaatc ccaccataag 120
aaatcgaacg gaggaggga gtggtcgtgc atcgattcct gttgttggtt cattgggtgt 180
gtgtgtgtaa cctggtggtt tcttctcttc ctttacaacg caatgcctgc gagcttcctt 240
cagtatgtaa cggagcgaat cacgggtcct ttgctgacc cgcccggtgt taagctcaaa 300
aaagaaggtc ttaaggcgaa acatcctgtt gtcttcattc ctgggattgt caccgggtggg 360
ctcgagcttt gggaaggcaa acaatgcgct gatgggttat ttagaaaacg tttgtggggg 420
ggaacttttg gtgaagtcta caaaagggtga gctcaacaat tctcactcct cctttatatt 480
gggattttgga ttggatctga tgagatcacg cacttggtgc ttcttcaaca tcaactcaaa 540
tttaattcca tgtttgtctg tcttactcct tacttttttt tttttttgat gtgaaacgct 600
attttcttaa gagactattt ctgtatgtgt aaggtaaagc ttccaaggac gtaattggct 660
tggactattt ctggtttgat gtttaacttta ggatataaaa tagctgcctt ggaatttcaa 720
gtcatcttat tgccaaatct gttgctagac atgcccctaga gtccgttcat aacaagttac 780
ttcctttact gtcgttgctg gtagatttag ctttctgtag cgtataatga agtagtggtt 840
tatgttttgt tgggaataga gaagttctaa ctacatctgt ggaaagtgtg ttcaggctgt 900
gatagaggac tgttgcttta ttattcaact atgtatctgt gtaattaaag ctagtctcct 960
tttgatcttt cagctcaatg tgcttttctc aatttttttc tcaatttcaa agtttcacat 1020
cgagtttatt cacatgtctt gaatttcgtc cactctcgtt ctgttatcca gctttgaact 1080
cctcccgaac ctgctatgga tatattaaaa aaaaagtggt ttgtgggttg catctttgtt 1140
acgatctgca tcttcttctt tcggctcagt gttcatgttt ttgctatggt agagatgggc 1200
aatgttattg ttgattgtaa cagtggata gttgatatga tcttaactaa tcaattatct 1260
ctttgattca ggctctatg ttgggtggaa cacatgtcac ttgacaatga aactgggttg 1320
gatccagctg gtattagagt tcgagctgta tcaggactcg tggctgctga ctactttgct 1380
cctggctact ttgtctgggc agtgctgatt gctaaccctg cacatattgg atatgaagag 1440
aaaaatatgt acatggctgc atatgactgg cggctttcgt ttcagaacac agaggttctt 1500
ttctcatcgt tctttctatt attctgttcc atgttacgtt tctttcttca ttacttaagg 1560
cttaaatatg tttcatgttg aattaatagg tacgtgatca gactcttagc cgtatgaaaa 1620
gtaatataga gttgatggtt tctaccaaac gtggaaaaaa agcagttata gttccgcatt 1680
ccatgggggtt cttgtatttt ctacatttta tgaagtgggt tgaggcacca gctcctctgg 1740
gtggcgggggg tgggcccagat tgggtgcaa agtatattaa ggcgggtgatg aacattgggtg 1800
gaccatttct tgggtgtcca aaagctgttg cagggttttt ctctgctgaa gcaaaggatg 1860
ttgcagttgc cagggtattga atactctgct atacttttga tgatcagaac cttggctctg 1920
gaactcaaag ttattctact aaatatcaat tctaataaca ttgctatatt atcgctgcaa 1980
ctgacattgg ttgattattt ttgctgctta tgtaactgaa actctcttga gattagacaa 2040
atgatgaatt gataattctt acgcattgct ctgtgatgac cagtttctta gcttcgacga 2100
taacatttgt catactgtct tttggagggc attgaatttt gctatggaaa gcgctggagc 2160
ttccatgctt gcattcttta ccaatttagc ttattctgct tctttcaatt ttcttgata 2220
tgcatctatg tctttttatt tcttcttaat taaagactcg ttggattagt tgctctatta 2280
gtcacttggt tcttaatat agaactttac tttcttcgaa aattgcagag cgattgcccc 2340
aggattctta gacaccgata tatttagact tcagaccttg cagcatgtaa tgagaatgac 2400
acgcacatgg gactcaacaa tgtctatgtt accgaaggga ggtgacacga tatggggcgg 2460
gcttgattgg tcaccggaga aaggccacac ctgttggtggg aaaaagcaaa agaacaacga 2520
aacttggtgt gaagcaggtg aaaacggagt ttccaagaaa agtctgttta actatggaag 2580
gatgatattt tttgggaaag aagtagcaga ggctgcgcca tctgagatta ataattattga 2640
ttttcgagta aggacatata aatcataata aaccttgtag attttctgat tgtatgatga 2700
atatctgtac attttatctg gtgaagggtg ctgtcctaat tcagagtatc ccaaatcaca 2760
cctgtcgtga cgttggtgaca gagtaccatg acatgggaat tgctgggatc aaagctatcg 2820
ctgagtataa ggtctacact gctggtgaag ctatagatct actacattat gttgctccta 2880

Cl
Cont

```

agatgatggc gcgtgggtgcc gctcatttct cttatggaat tgctgatgat ttggatgaca 2940
ccaagtatca agatcccaaa tactgggtcaa atccgtaga gacaaagtaa gtgatttctt 3000
gattccaact gtatccttcg tcctgatgca ttatcagtct ttttgtttctt ggtccttggtg 3060
gatatggttt tcagctcaaa gcttacaagg ctgtttctga gcctttctca aaaaggcttg 3120
ctcagtaata ttgaggtgct aaagttgata catgtgactc ttgcttataa atcctccgtt 3180
tggtttggtc tgctttttca gattaccgaa tgctcctgag atggaaatct actcattata 3240
cggagtgggg ataccaacgg aacgagcata cgtatacaag ctttaaccagt ctcccagacg 3300
ttgcatcccc tttcagatat tcacttctgc tcacgaggag gacgaagata gctgtctgaa 3360
agcaggagtt tacaatgtgg atggggatga aacagtaccc gtccctaagtg ccgggtacat 3420
gtgtgcaaaa gcgtggcgtg gcaagacaag attcaaccct tccggaatca agacttatat 3480
aagagaatac aatcactctc cgccggctaa cctgttgtaa gggcgcgga cgcagagtgg 3540
tgcccatgtt gatatcatgg gaaactttgc tttgatcgaa gatatcatga gggttgccgc 3600
cggaggtaac ggggtctgata taggacatga ccaggtccac tctggcatat ttgaatggtc 3660
ggagcgtatt gacctgaagc tgtga 3685

```

<210> 5b
 <211> 402
 <212> DNA
 <213> *Arabidopsis thaliana*

<220>
 <221> CDS
 <222> (120)..(401)

<221> Unsure
 <222> 1..401
 <223> n is c, g, a, t or u.

<221> Unsure
 <222> 1..401
 <223> Xaa = unknown

<400> 5b

agaaacagct ctttgtctct ctcgactgat ctaacaatcc ctaatctgtg ttctaaattc 60
 ctggacgaga ttgacaaaag tccgtatagc ttaacctggg ttaatttcaa gtgacagat 119
 atg ccc ctt att cat cgg aaa aag ccg acg gag aaa cca tcg acg ccg 167
 Met Pro Leu Ile His Arg Lys Lys Pro Thr Glu Lys Pro Ser Thr Pro
 1 5 10 15
 cca tct gaa gag gtg gtg cac gat gag gat tcg caa aag aaa cca cac 215
 Pro Ser Glu Glu Val Val His Asp Glu Asp Ser Gln Lys Lys Pro His
 20 25 30
 gaa tct tcc aaa tcc cac cat aag naa tcg aac gga gga ggg aag tgg 263
 Glu Ser Ser Lys Ser His His Lys Xaa Ser Asn Gly Gly Gly Lys Trp
 35 40 45
 tcg tgc atc gat tct tgt tgt tgg ttc att ggg tgt gtg tgt gta acc 311
 Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr
 50 55 60
 tgg tgg ttt ctt ctc ttc ctt tac aac gca atg cct gcg agc ttc cct 359
 Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro
 65 70 75 80

C1
 Cont

cag tat gta acg gag ccg aat cac gng tcc ttt gcc tta ccc g 402
 Gln Tyr Val Thr Glu Pro Asn His Xaa Ser Phe Ala Leu Pro
 85 90

<210> 6b
 <211> 643
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)..(402)

<400> 6b

cgg gag aaa ata gct gct ttg aag ggg ggt gtt tac tta gcc gat ggt 48
 Arg Glu Lys Ile Ala Ala Leu Lys Gly Gly Val Tyr Leu Ala Asp Gly
 1 5 10 15

gat gaa act gtt cca gtt ctt agt gcg ggc tac atg tgt gcg aaa gga 96
 Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly
 20 25 30

tgg cgt ggc aaa act cgt ttc agc cct gcc ggc agc aag act tac gtg 144
 Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
 35 40 45

aga gaa tac agc cat tgc cca ccc tct act ctg ctg gaa ggc agg ggc 192
 Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
 50 55 60

acc cag agc ggt gca cat gtt gat ata atg ggg aac ttt gct cta att 240
 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
 65 70 75 80

gag gac gtc atc aga ata gct gct ggg gca acc ggt gag gaa att ggt 288
 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
 85 90 95

ggc gat cag gtt tat tca gat ata ttc aag tgg tca gag aaa atc aaa 336
 Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys
 100 105 110

ttg aaa ttg taa cct atg gga agt taa aga agt gcc gac ccg ttt att 384
 Leu Lys Leu Pro Met Gly Ser Arg Ser Ala Asp Pro Phe Ile
 115 120 125

gcg ttc caa agt gtc ctg cctgagtgcg actctggatt ctgcttaaatt 432
 Ala Phe Gln Ser Val Leu
 130

attgtaattt ttcacgcttc attcgtccct ttgtcaaatt tacatttgac aggacgcaa 492
 tgcgatacga tggtgtaccg ctattttcag cattgtatat taaactgtac aggtgtaagt 552
 tgcatttgcc agctgaaatt gtgtagtcgt tttctttacg atttaatanc aagtggcgga 612

C1
 Cont

gcagtgcccc aagcnaaaaa aaaaaaaaaa a

643

<210> 7b
 <211> 115
 <212> PRT
 <213> Zea mays

<400> 7b

Arg	Glu	Lys	Ile	Ala	Ala	Leu	Lys	Gly	Gly	Val	Tyr	Leu	Ala	Asp	Gly
1				5				10						15	
Asp	Glu	Thr	Val	Pro	Val	Leu	Ser	Ala	Gly	Tyr	Met	Cys	Ala	Lys	Gly
		20					25					30			
Trp	Arg	Gly	Lys	Thr	Arg	Phe	Ser	Pro	Ala	Gly	Ser	Lys	Thr	Tyr	Val
		35				40					45				
Arg	Glu	Tyr	Ser	His	Ser	Pro	Pro	Ser	Thr	Leu	Leu	Glu	Gly	Arg	Gly
	50					55				60					
Thr	Gln	Ser	Gly	Ala	His	Val	Asp	Ile	Met	Gly	Asn	Phe	Ala	Leu	Ile
65				70				75						80	
Glu	Asp	Val	Ile	Arg	Ile	Ala	Ala	Gly	Ala	Thr	Gly	Glu	Glu	Ile	Gly
		85						90						95	
Gly	Asp	Gln	Val	Tyr	Ser	Asp	Ile	Phe	Lys	Trp	Ser	Glu	Lys	Ile	Lys
		100						105						110	
Leu	Lys	Leu													
		115													

<210> 8b
 <211> 516
 <212> DNA
 <213> Neurospora crassa

<220>
 <221> Unsure
 <222> 1..516
 <223> n is g, c, a, t, or u.

<400> 8b

ggtggcgaag	acganggcgg	aagttggagg	ctaacgagaa	tgacnctcgg	agatggatct	60
accctctaga	gacacgacta	ccnttgacc	cagcctcaag	gtntacngtt	tntatgggta	120
ggaagccgac	ggagcgagcc	tacatctatc	tggcgcccga	tcccgggacg	acaacgcac	180
tttagatgac	gatcgatacg	actttgactn	aggggcacat	tgaccacggg	gtgattttgg	240
gcgaaggcga	tggcacagtg	aaccttatga	gtttggggta	cctgtgcaat	aaggggtgga	300
aaatgaagag	atacaatcct	gcgggctcaa	aaataaccgt	ggtcgagatg	ccgcatgaac	360
cagaacgggt	caatccgaga	ggagggccga	atacggcgga	cttaaataatg	tagaaaaggt	420
tgaaatttat	gaagagtaat	taaatacggc	acatagggtta	ctcaatagta	tgactaatta	480
aaaaaaaaatt	ttttttctaa	aaaaaaaaaa	aaaaaa			516

<210> 9b
 <211> 1562
 <212> DNA
 <213> Arabidopsis thaliana

<400> 9b

C1
Cont

atgaaaaaaa tatcttcaca ttattcggta gtcatagcga tactcgttgt ggtgacgatg 60
 acctcgatgt gtcaagctgt gggtagcaac gtgtaccctt tgattctggt tccaggaaac 120
 ggaggttaacc agctagaggt acggctggac agagaatata agccaagtag tgtctgggtgt 180
 agcagctggt tatatccgat tcataagaag agtgggtgat ggtttaggct atgggtcgtat 240
 gcagcagtgt tattgtctcc cttcaccagg tgcttcagcg atcgaatgat gttgtactat 300
 gacctgattt tggatgatta ccaaaatgct cctgggtgct aaacccgggt tccctcattt 360
 ggttcgacca aatcacttct atacctcgac cctcgtctcc ggtagtagtact ttccaagata 420
 tatcattttt ggacatttgc ataatagaac aaatagacat aaatttgggg gattattggt 480
 atatcaatat ccattttatat gctagtcggt aatgtgagt ttatgttagt atagttaatg 540
 tgagtgttat gtgattttcc attttaaatg aagctagaaa gttgtcgttt aataatgttg 600
 ctatgtcatg agaattataa ggacactatg taaatgtagc ttaataataa ggtttgattt 660
 gcagagatgc cacatcttac atggaacatt tggtgaaagc tctagagaaa aaatgcgggt 720
 atgttaacga ccaaaccatc ctaggagctc catatgattt caggtagcggc ctggctgctt 780
 cgggccaccc gtcccgtgta gcctcacagt tctacaaga cctcaaaca ttggtggaaa 840
 aaactagcag cgagaacgaa ggaaagccag tgatactcct ctcccatagc ctaggaggac 900
 ttttcgtcct ccatttcttc aaccgtacca ccccttcctg gcgcccgaag tacatcaaac 960
 actttgttgc actcgtctgc ccattgggtg ggaagatctc tcagatgaag acatttgctt 1020
 ctggcaacac actcgggtgt ccttttagtta accctttgct ggtcagacgg catcagagga 1080
 cctccgagag taaccaatgg ctacttccat ctaccaaagt gtttcacgac agaactaac 1140
 cgcttgctgt aactccccag gtttaactaca cagcttacga gatggatcgg ttttttgcag 1200
 acattggatt ctcaacaagg gttgtgcctt acaagacaag agtgttgctt ttaacagagg 1260
 agctgatgac tccgggagtg ccagtcactt gcataatagg gagaggagtt gatacaccgg 1320
 aggttttgat gtatggaaaa ggaggattcg ataagcaacc agagattaag tatggagatg 1380
 gagatgggac ggttaatttg gcgagcttag cagctttgaa agtcgatagc ttgaacaccg 1440
 tagagattga tggagtttcg catacatcta tacttaaaga cgagatcgca cttaaagaga 1500
 ttatgaagca gatttcaatt attaatatg aattagocaa tgtaaatgcc gtcaatgaat 1560
 ga 1562

<210> 10b

<211> 3896

<212> DNA

<213> Arabidopsis thaliana

<400> 10b

atgggagcga attcgaaatc agtaacggct tccttcaccg tcatcgccgt ttttttcttg 60
 atttgcggtg gccgaactgc ggtggaggat gagaccgagt ttcacggcga ctactcgaag 120
 ctatcggtga taatcattcc gggatttgcg tcgacgcagc tacgagcgtg gtcgatcctt 180
 gactgtccat acactccgtt ggacttcaat ccgctcgacc tcgtatggct agacaccact 240
 aagggtccgtg atcttcattt ccttcgctcc ttattctgtc ggtcagatca cttgttgatg 300
 aattccaagc gaaatatagc aatgaagcat gtctcgtctc tcttattgat tcgttcatta 360
 gtcaacagtg acgcttctga atctgagttt agagtcatat aaaacagctg actcggcgag 420
 tgtttcccat cgcttttggg tcgctaaatg tagcgcaatg aatgtgtaat tagtctgcgc 480
 tttttattca actagatctg caagtttttc agagtgtca atagtagtta gaaaatgtta 540
 ggtcatttta cttgtgcatt gtgattcttt tgggtgttgc ttactgatcg acgtgatgga 600
 tggtttacag cttctttctg ctgtcaactg ctggtttaag tgtatggtgc tagatcctta 660
 taatcaaaca gaccatcccg agtgaagtc accggcctgac agtgggtctt cagccatcac 720
 agaattggat ccaggttaca taacaggtag ttccggattt ttctttcttt tgagttttct 780
 tcaatttgat atcatcttgt tgtgatataa tatggctaag ttcattaatt tgggtcaatt 840
 tcaggtcttc tttctactgt ctggaaagag tggcttaagt ggtgtgttga gtttggata 900
 gaagcaaatg caattgtcgc tgttccatac gattggagat tgtcaccaac caaattggaa 960
 gagcgtgacc tttactttca caagctcaag ttagtcctta tcaggtcaat gtcttttatc 1020
 ttctcttttt atgtaagata agctaagagc tctggctcgtc ttcttttttg cagggtgacc 1080
 tttgaaactg ctttaaaact ccgtggcggc ccttctatag tatttgccea ttcaatgggt 1140
 aataatgtct tcagatactt tctggaatgg ctgaggctag aaattgcacc aaaacattat 1200
 ttgaagtggc ttgatcagca tatccatgct tatttcgctg ttggtaccgg cctactatcc 1260
 ttaagttacc attttatttt ttctctaatt gggggagtta tgttggact tactggattg 1320
 agctcgatac ctgatttggt gttgatttag gagtcctct tcttgggtct gttgaggcaa 1380

C1
Cont

tcaaattctac tctctctggt gtaacgtttg gccttctctg ttctgaggtg acctctgact 1440
 tctcttttagt ttttaagtagt tgatatcaac caggtcttat aactcactgg attttctttt 1500
 tgaaagtatt acttttggtta attgaactgc tgtacgcgat atggtatctg tagatcttga 1560
 agtgctagtt atcaaagaac atattgtggg tagtatacct gtcagcggcc ttagctaata 1620
 caaccaaacc acatgtacac tgatttagtt ttcagattat tatggtagac ttttaagttga 1680
 gaagaaactt tgactgaaat ctttttattt taataggcta tgatttgttt attgaaatca 1740
 tgtgacatat tgacatgcgc ttctcatggt ttttgttggc aaggcttcag ggaactgctc 1800
 ggttggtgtc caattctttt gcgtcgtcat tgtggcttat gccattttca aagaattgca 1860
 aggggtgataa cacattctgg acgcattttt ctgggggtgc tgcaaagaaa gataagcgcg 1920
 tataccactg tgatgaagag gaatatcaat caaaatatc tggctggccg acaaattata 1980
 ttaacattga aattccttcc actagcgggt agactctgta tatgcaactg taacactaac 2040
 aaaagtttca ccaagaatgt tcaactctcat atttcgttcc tttgatgtgt atccatcagt 2100
 tacagaaaca gctctagtca acatgaccag catggaatgt ggccttccca cccttttgtc 2160
 tttcacagcc cgtgaactag cagatgggac tcttttcaaa gcaatagaag actatgacc 2220
 agatagcaag aggatgttac accagttaaa gaagtacgta cctttctttg tgataagaaa 2280
 tattgctcat cgatcatcac ttgctggctt cttgtacgtc aaattgtttt gtttaaactc 2340
 ctatatcaat tgttcatatg ctttgtcttt ctactataa gaaacaagta taatcagaaa 2400
 ccttattatt gattatcagt tctctcctta tattatggaa tgtctttttc gtttacagtt 2460
 atgaatgcaa aaggggggat tttagttgat tgattctctc attctctagt ttgttttgac 2520
 taatagcgtc aattttgttt ttctagcaaa tctttgtgaa ttatatataa catgctaact 2580
 atacttttca ggttgatca tgatgaccct gtttttaate ctctgactcc ttgggagaga 2640
 ccacctataa aaaatgtatt ttgcatatat ggtgctcatc taaagacaga ggtatgatgc 2700
 attctcaata tcacattatg cgttgacttt gttattatat tccccatttg gtttgaacta 2760
 tctttttgaa ttatgattta tcttctccct tgcattctat gctattaagc gttaaaggta 2820
 ctaaattgat gaagctgtct gtcatagggt ggttattact ttgccccaaag tggcaaacct 2880
 tatectgata attggatcat cacggatata atttatgaaa ctgaagggtc cctcgtgtca 2940
 aggtaatttt ccgcaatggc agaagtaaaa caggaaggca aagtcttctg tatcagtcta 3000
 gtggcatgtt atctcagttg cataagcaaa ttattaaaca actaaaattt aagtactttt 3060
 ttatcattcc ttttgagctt agtggaatgat cagtgctta aagtgggaag aggtgttgca 3120
 tgaaacatga cacttgatc aaagataact agcaaaacaa aactaaccca tttctgaatt 3180
 tcatattatt aggagtagtc gtgcttttaa aaaatttgtt ttaagaaacc gaaaaactag 3240
 ttcatactct gattgtgcaa tatctgcagg tctggaactg tggttgatgg gaacgctgga 3300
 cctataactg gggatgagac ggtaagctca gaagttggtt ttgaaattat cttcttgcaa 3360
 actactgaag actaagataa tacttgcttc tggaaactg cttgctatgt tctctagtac 3420
 actgcaatat tgactctccg ctacttttat tgattatgaa attgatctct tataggtacc 3480
 ctatcattca ctctcttggt gcaagaattg gctcggacct aaagttaaca taacaatggc 3540
 tccccaggta ctctttttta gttcctcacc ttatatagat caaactttaa gtgtactttt 3600
 ctggttatgt gttgatttac ctccaatttg ttctttctaa aaatcatata tctctgtact 3660
 cctcaagaac ttgtattaat ctaaagcaga ttctcatgg gaaaataaaa caacagccag 3720
 aacacgatgg aagcgacgta catgtggaac taaatgttga tcatgagcat gggtcagaca 3780
 tcatagctaa catgacaaaa gcaccaaggg ttaagtacat aaccttttat gaagactctg 3840
 agagcattcc ggggaagaga accgcagctc gggagcttga taaaagtggg tattaa 3896

<210> 11b
 <211> 709
 <212> DNA
 <213> tomato

<400> 11b

ctggggccaa aagtgaacat aacaaggaca ccacagtcag agcatgatgt tcagatgtac 60
 aagtgcattc aaatatagag catcaacatg gtgaagatat cattcccaat atgacaaagt 120
 tacctacaat gaagtacata acctattatg aggattctga aagttttcca gggacaagaa 180
 cagcagtttg ggagcttgat aaagcaaatc acaggaacat tgtcagatct ccagctttga 240
 tgcgggagct gtggcttgag atgtggcatg atattcatcc tgataaaaag tccaagtttg 300
 ttacaaaagg tgggtgtctga tctcactaat tttctctat aaatgtttga gtttgtattg 360
 acattgtaag tattgcaaca aaaagcaaaag cgtgggcctc tgagggatga ggactgctat 420
 tgggattacg ggaaagctcg atgtgcatgg gctgaacatt gtgaatacag gttagaatat 480

Sub D1
C1
Cmt

44

tcaaattata ttttgcaaaa tattctcttt ttgtgtattt aggccacctt tccccggtca 540
caacgatgca gatatgtatt cggggatggt cacctgggac agagttgcag attgaagagt 600
tctacatctc acatcctgtc aactatgtg tgatatttaa gaaactttgt ttggcggaac 660
aacaagtttg cacaacatt tgaagaagaa agcgaaatga ttcagagag 709
